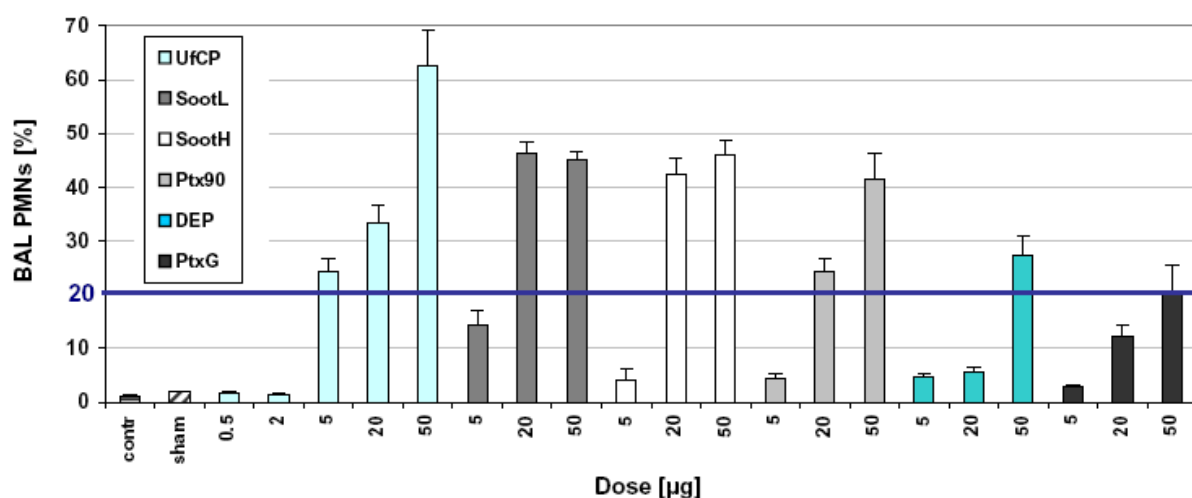


Supplemental Material, Table 1

RefSeq	Gene Name	Gene Abbr.	Forward Primer Sequence	Reverse Primer Sequence
NM_007436	aldehyde dehydrogenase family 3, subfamily A 1	Aldh3a1	AGC TCC CAC CAT CCT AGT	GTC A TT GGC TGT CAC TCC
NM_009969	colony stimulating factor 2 (granulocyte-macrophage)	Csf2	GCC ATC AAA GAA GCC CTG AA	GCG GGT CTG CAC ACA TGT TA
NM_008176	chemokine (C-X-C motif) ligand 1	Cxc/1	CCG AAG TCA TAG CCA CAC	GTG CCA TCA GAG CAG TCT
NM_009141	chemokine (C-X-C motif) ligand 5	Cxc/5	GAC TCT GAC CCC AGT GAA G	GTG AGA TGA GCA GGA AGC
NM_009992	cytochrome P450, family 1, subfamily a, polypeptide 1	Cyp1a1	GCT GGG TTT GAC ACA GTC	ATA GGG CAG CTG AGG TCT
NM_009994	cytochrome P450, family 1, subfamily b, polypeptide 1	Cyp1b1	GCC TCA GGT GTC TAG GTC T	GTG GAC TGT CTG CAC TAA GG
NM_010295	glutamate-cysteine ligase, catalytic subunit	Gclc	GGA GAC CAG AGT ATG GGA GT	AGC CTA GTC TGG GGA ATG
NM_008160	glutathione peroxidase 1	Gpx1	GGG ACT ACA CCA AGA TGA	CAG GTC GGA CGT ACT TGA
NM_001037741	glutathione peroxidase 4	Gpx4	AGC CCC AGG TGA TAG AGA	CCT GCC GTG CTA TCT CTA
NM_010344	glutathione reductase 1	Gsr	AGG GCC ACA TCC TAG TAG AC	GTG GCT GAA GAC CAC AGT AG
NM_008181	glutathione S-transferase, alpha-1	Gsta1	AGG AGA GAG CCC TGA TTG	CTG TTG CCC ACA AGG TAG
NM_010442	heme oxygenase (decycling) 1	Hmox1	AGG TGA TGC TGA CAG AGG	GTG TCT GGG ATG AGC TAG TG
NM_010479	heat shock protein 1 A	Hspa1a	GAC AAG TCG GAG AAC GTG	GAG TAG GTG GTG AAG GTC TG
NM_008361	interleukin 1 beta	Il1b	CAA CCA ACA AGT GATATT CTC CAT G	GAT CCA CAC TCT CCA GCT GCA
NM_031168	interleukin 6	Il6	GTT CTC TGG GAA ATC GTG GA	TGT ACT CCA GGT AGC TAT GG
NM_013599	matrix metalloproteinase 9	Mmp9	GAA GTG GGG TTT CTG TCC	AGC CCT CGA GGT AGC TAT AC
NM_013602	metallothionein 1	Mt1	GGT CTT CTC TGT TGG GGA CA	GCT GGG TTG GTC CGA TAC TA
NM_008630	metallothionein 2	Mt2	TAG ATG GAT CCT GCT CCT GC	CAC TTG TCG GAA GCC CTC TT
NM_008706	NAD(P)H dehydrogenase, quinone 1	Nqo1	CAG GTG AGC TGA AGG ACT C	CCT GCT ACG AGC ACT CTC T
NM_010957	8-oxoguanine DNA-glycosylase 1	Ogg1	GAG ACT GCT GAG ACA AGA CC	GTG AGT CTC TGC TTC TGG AC
NM_011198	cyclooxygenase 2; COX2 (mitogen-inducible)	Ptgs2	CAA CAC CTG AGC GGT TAC	GTT CCA GGA GGA TGG AGT
NM_013693	tumor necrosis factor	Tnfa	CAC CAC GCT CTT CTG TCT	GGC TAC AGG CTT GTC ACT
NT_039649.7	18S ribosomal RNA	Rn18s	GAC TGT CTC GCC GGT GTC	GGA GAG CCG GAA CGT CGA

List of genes with the respective primer pairs used for the quantitative PCR analysis. Transcript sequences are identified by the NCBI Reference Sequences ID. All genes are abbreviated by their official MGI symbol (Mouse Genome Informatics, <http://www.informatics.jax.org>). Primer were derived by Primer3 open source software, (<http://primer3.sourceforge.net/>) using the primer picking conditions: GC: 55-60%; annealing: 55°C.

Supplemental Material, Figure 1



The data point '50ug UfCP' deviates by 13% (55.1% now 62.5%) from Stoeger et al. (2006) due to an averaging error

Inflammatory dose response in lungs of mice (n = 8) 24h after particle instillation. Polymorphonuclear leucocytes (PMNs) recovered by BAL are given as percentage of total BAL cells. The inflammatory efficacy of the particles was defined as the 20% PMN effect level (blue line) divided by the particle mass causing this effect level. The respective mass values were derived by linear interpolation between the data points of the dose response relations (Table 1).

Supplemental Material, Figure 2

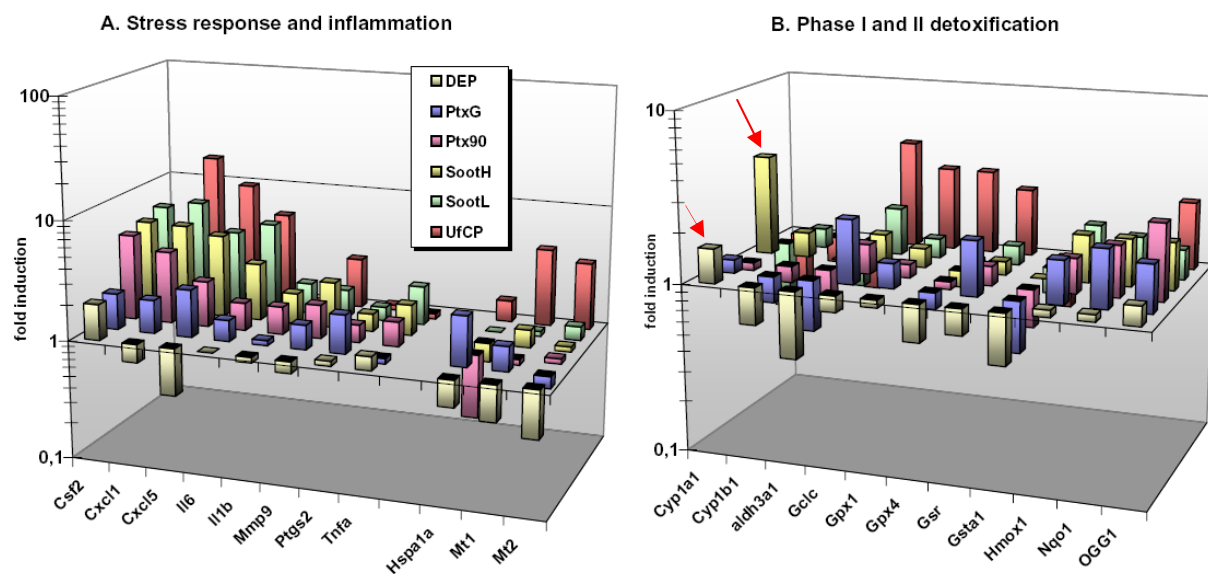


Illustration of gene expression (mRNA levels) of selected marker enzymes (Table 2) characterizing stress response and inflammation (A) as well as phase I and II detoxification (B). cDNA samples from four animals were pooled for quantitative PCR analysis. Expression levels were normalized to 18S rRNA and displayed as fold induction relative to sham control mice. The red arrows indicate the 1.6 and 3.9 fold induction of Cyp1a1 by DEP and SootH particle instillation.